

AMENDMENT

Please amend the application as indicated hereafter.

In the Specification

In the paragraph on page 7, lines 18-21:

The phrase "marker sequence" or "marker" refers to a genetic sequence (i.e., DNA found on a chromosome) that has more than one variant in the general population. Because an organism generally has two ~~to~~ copies of each chromosome, the organism will have two copies of each marker, which may be the same or different from each other.

In the paragraph on page 13, lines 6-12:

In more detail, as discussed above, markers near to disease alleles tend to come from the same founder and tend to pass along with the disease alleles. As a result, the same pattern of marker alleles as found in the founder should tend to be more prevalent in affected people. Thus, in the example shown in FIG. 2, affected ~~effect~~ persons should have alleles BB for marker 10 and alleles AA for marker ~~markers~~ 11 much more frequently than other combinations of markers. Accordingly, particular combinations of homozygous markers that occur more frequently than other combinations of markers are of particular interest.

In the paragraph on page 19, lines 1-2:

Fourth, the ratio of $\Pr(O \mid \text{autozygous})$ to $\Pr(O \mid \text{not autozygous})$ is computed for each marker. Preferably ~~Preferable~~, a log base 10 is taken of each ratio. More formally: